What is claimed is:

1. A method for predicting single nucleotide polymorphisms, comprising the steps of:

obtaining a variation predictiveness matrix; and

predicting one or more single nucleotide polymorphisms of a nucleic acid sequence based on the variation predictiveness matrix.

2. The method of claim 1 further comprising one or more nucleic acid sequences with chemical modifications.

3. The method of claim 2, wherein the chemical modifications include methylation or other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid sequence as a whole.

4. The method of claim 1, wherein the step of predicting the likelihood of one or more single nucleotide polymorphisms comprises the steps of:

comparing the nucleic acid sequence one or more bases at a time with the variation predictiveness matrix to assign a variation value to bases in the nucleic acid sequence; and

selecting the polymorphisms that will likely cause a variation in one or more bases of the nucleic sequence based on the variation value.

5. The method of claim 4, wherein the variation in one or more bases is nonsynonymous.

6. The method of claim 4, wherein the variation in one or more bases is synonymous.

7. The method of claim 1, further comprising the step of generating a dataset of single nucleotide polymorphisms for one or more nucleic acid sequences.

8. The method of claim 1, wherein the step of obtaining a variation predictiveness matrix, further comprises the steps of:

calculating a variation frequency from a first base to a second base in a dataset of two or more genes; and

generating the variation predictiveness matrix from the calculated variation frequency.

9. The method of claim 8 wherein the dataset comprises genes with nucleic acid chemical modifications.

10. The method of claim 9, wherein the chemical modifications include methylation or other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid as a whole.

11. The method of claim 8, wherein the variation frequency is determined from a known mutation dataset.

12. The method of claim 8, wherein the variation frequency is determined from a dataset of known diseases.

13. The method of claim 8, wherein the variation frequency is determined from a dbSNP database.

14. The method of claim 8, wherein the variation frequency is determined from a non-human mutation database.

15. The method of claim 8, wherein the variation frequency is determined from a disease-specific database.

16. The method of claim 8, wherein the variation frequency is determined from a non-human disease database.

17. The method of claim 8, wherein the variation frequency is determined from a HGMD database.

18. The method of claim 8, wherein the variation frequency is determined from a linkage database.

19. The method of claim 8, wherein the variation frequency is determined from a splice variant database.

20. The method of claim 8, wherein the variation frequency is determined from a translocation database.

21. The method of claim 8, wherein the variation frequency is determined from a database of known mutations.

22. The method of claim 8, wherein the variation frequency is further adjusted for wild type genes.

23. The method of claim 8, wherein the variation frequency is further adjusted for engineered or non-naturally occurring genes.

24. The method of claim 8, wherein the variation frequency is further adjusted for conservative polymorphisms.

25. The method of claim 8, wherein the variation frequency is further adjusted for non-conservative polymorphisms.

26. The method of claim 8, wherein the variation frequency is further adjusted for cDNA stability.

27. The method of claim 8, wherein the variation frequency is further adjusted for predicted DNA structure.

28. The method of claim 8, wherein the variation frequency is further adjusted for predicted RNA structure.

29. The method of claim 8, wherein the variation frequency is further adjusted for predicted protein structure.

30. The method of claim 8, wherein the variation frequency is further adjusted for post-translational modification sequences.

31. The method of claim 8, wherein the variation frequency is further adjusted for protein stability.

32. The method of claim 8, wherein the variation frequency is further adjusted for predicted protein transport.

33. The method of claim 8, wherein the variation frequency is further adjusted for shuffled genes.

34. The method of claim 8, wherein the variation frequency is further adjusted for site-directed mutagenesis genes.

35. The method of claim 8, wherein the variation frequency is further adjusted for methylated sequences

36. The method of claim 8, wherein the variation frequency is further adjusted for epigenetic variation.

37. The method of claim 8, wherein the nucleic acid sequence comprises a cDNA sequence.

38. The method of claim 8, wherein the nucleic acid sequence comprises genomic sequence.

39. The method of claim 8, wherein the nucleic acid sequence comprises an intron/exon boundary.

40. The method of claim 8, wherein the nucleic acid sequence comprises a transcriptional control sequence.

41. The method of claim 8, wherein the nucleic acid sequence comprises a transport control sequence.

42. The method of claim 8, wherein the nucleic acid sequence comprises a translational control sequence.

43. The method of claim 8, wherein the nucleic acid sequence comprises a transcriptional control sequence.

44. The method of claim 8, wherein the nucleic acid sequence comprises a splicing control sequence.

45. The method of claim 1, wherein the step of obtaining a variation predictiveness matrix correlates the frequency of a first codon mutation to a second codon mutation with a variation predictiveness value of a nucleic acid sequence from one to ten bases at a time.

46. The method of claim 1, wherein in the variation predictiveness matrix is normalized for the codon usage of a target organism.

47. The method of claim 1, wherein the variation predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database.

48. The method of claim 1, wherein the variation predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database minus the known mutant genes of the mutant gene dataset.

49. The method of claim 1, where the nucleic acid sequence comprises an entire genome.

50. The method of claim 1, where the nucleic acid sequence comprises a human genome.

51. The method of claim 1, where the nucleic acid sequence comprises a gene cluster for a target human disease.

52. The method of claim 1, where the variation predictiveness matrix is based on a mutant gene dataset that comprises a human mutation database.

53. The method of claim 1, wherein the steps are affected by a computer program.

54. The method of claim 53, wherein the computer program is SNIDE.

55. The method of claim 53, wherein the computer program is SNooP.

56. The method of claim 1, wherein the variation predictiveness matrix is determined in silico from a human mutant database.

57. The method of claim 1, wherein the step of predicting a likelihood of one or more single nucleotide polymorphisms is determined in silico.

58. A method for creating a variation predictiveness value for use in a variation predictiveness matrix, comprising the steps of:

calculating the variation frequency from a first nucleic acid to a second nucleic acid in a dataset of two or more variations; and

determining a variation predictiveness value from the calculated variation frequency.

59. The method of claim 58, further comprising the step of generating a variation predictiveness matrix that correlates the frequency of a first to a second variation with the variation predictiveness value.

60. The method of claim 58, wherein the dataset comprises genes with nucleic acid chemical modifications.

61. The method of claim 60, wherein the chemical modifications include methylation or other chemical groups that incorporate additional charge, polarizability,

hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid as a whole.

62. The method of claim 58, wherein the variation frequency is determined from a known mutation dataset.

63. The method of claim 58, wherein the variation frequency is determined from a dataset of known diseases.

64. The method of claim 58, wherein the variation frequency is determined from a dbSNP database.

65. The method of claim 58, wherein the variation frequency is determined from a non-human mutation database.

66. The method of claim 58, wherein the variation frequency is determined from a disease-specific database.

67. The method of claim 58, wherein the variation frequency is determined from a non-human disease database.

68. The method of claim 58, wherein the variation frequency is determined from a HGMD database.

69. The method of claim 58, wherein the variation frequency is determined from a linkage database.

70. The method of claim 58, wherein the variation frequency is determined from a splice variant database.

71. The method of claim 58, wherein the variation frequency is determined from a translocation database.

72. The method of claim 58, wherein the variation frequency is determined from a database of known mutations.

73. The method of claim 58, wherein the variation frequency is further adjusted for wild type genes.

74. The method of claim 58, wherein the variation frequency is further adjusted for engineered or non-naturally occurring genes.

75. The method of claim 58, wherein the variation frequency is further adjusted for conservative polymorphisms.

76. The method of claim 58, wherein the variation frequency is further adjusted for non-conservative polymorphisms.

77. The method of claim 58, wherein the variation frequency is further adjusted for cDNA stability.

78. The method of claim 58, wherein the variation frequency is further adjusted for predicted DNA structure.

79. The method of claim 58, wherein the variation frequency is further adjusted for predicted RNA structure.

80. The method of claim 58, wherein the variation frequency is further adjusted for predicted protein structure.

81. The method of claim 58, wherein the variation frequency is further adjusted for post-translational modification sequences.

82. The method of claim 58, wherein the variation frequency is further adjusted for protein stability.

83. The method of claim 58, wherein the variation frequency is further adjusted for predicted protein transport.

84. The method of claim 58, wherein the variation frequency is further adjusted for shuffled genes.

85. The method of claim 58, wherein the variation frequency is further adjusted for site-directed mutagenesis genes.

86. The method of claim 58, wherein the variation frequency is further adjusted for methylated sequences

87. The method of claim 58, wherein the variation frequency is further adjusted for epigenetic variation.

88. The method of claim 58, wherein the variations comprise a cDNA sequence.

89. The method of claim 58, wherein the variations comprise genomic sequence.

90. The method of claim 58, wherein variations comprise an intron/exon boundary.

91. The method of claim 58, wherein variations comprise exons.

92. The method of claim 58, wherein variations comprise other SNPs.

93. The method of claim 58, wherein variations comprise inversions.

94. The method of claim 58, wherein variations comprise deletions.

95. The method of claim 58, wherein variations comprise splice variations.

96. The method of claim 58, wherein variations comprise translocations.

97. The method of claim 58, wherein variations comprise a transcriptional control sequence.

98. The method of claim 58, wherein variations comprise a transport control sequence.

99. The method of claim 58, wherein variations comprise a translational control sequence.

100. The method of claim 58, wherein variations comprise a transcriptional control sequence.

101. The method of claim 58, wherein variations comprise a splicing control sequence.

102. The method of claim 59, wherein in the variation predictiveness matrix is normalized for the nucleotide usage of a target organism.

103. The method of claim 59, wherein the variation predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database.

104. The method of claim 58, wherein the variation predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database minus the known mutant genes of the mutant gene dataset.

105. The method of claim 58, where the nucleic acid comprises one or more bases.

106. The method of claim 58, where the nucleic acid comprises DNA.

107. The method of claim 58, where the nucleic acid comprises RNA.

108. The method of claim 58, where the nucleic acid comprises a triplet.

109. The method of claim 58, The method of claim 16, where the nucleic acid comprises a codon.

110. The method of claim 58, The method of claim 16, where the nucleic acid comprises one or more non-sequence base modifications.

111. The method of claim 58, where the nucleic acid comprises modified nucleic acids.

112. The method of claim 58, wherein modified nucleic acids include methylation or other chemical groups that incorporate additional charge, polarizability, hydrogen

bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid as a whole.

113. The method of claim 58, where the nucleic acid comprises an entire genome.

114. The method of claim 58, where the nucleic acid comprises a human genome.

115. The method of claim 58, where the nucleic acid comprises a gene cluster for a target human disease.

116. The method of claim 58, where the variation predictiveness matrix is based on a mutant gene dataset that comprises a human mutation database.

117. The method of claim 58, wherein the steps are affected by a computer program.

118. The method of claim 58, wherein the computer program is SNIDE.

119. The method of claim 58, wherein the computer program is SNooP.

120. The method of claim 58, wherein the variation predictiveness value is determined in silico from a human mutant database.

121. The method of claim 58, wherein the step of predicting a likelihood of one or more single nucleotide variation is determined in silico.

122. A method for creating a polymorphism predictiveness value for use in a mutation predictiveness matrix, comprising the steps of:

calculating the mutation frequency from a first codon to a second codon in a dataset of two or more mutant genes; and

determining a polymorphism predictiveness value from the calculated mutation frequency.

123. The method of claim 122, further comprising the step of generating a codon polymorphism predictiveness matrix that correlates the frequency of a first to a second codon mutation with the polymorphism predictiveness value.

124 The method of claim 122, wherein the dataset comprises nucleic acids with chemical modifications.

125 The method of claim 124, wherein the chemical modifications include methylation or other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid as a whole.

126 The method of claim 122, wherein the mutation frequency is determined from a known mutation dataset.

127 The method of claim 122, wherein the mutation frequency is determined from a dataset of known diseases.

128 The method of claim 122, wherein the mutation frequency is determined from a dbSNP database.

129 The method of claim 122, wherein the mutation frequency is determined from a non-human mutation database.

130 The method of claim 122, wherein the mutation frequency is determined from a disease-specific database.

131 The method of claim 122, wherein the mutation frequency is determined from a non-human disease database.

132. The method of claim 122, wherein the mutation frequency is determined from a HGMD database.

133. The method of claim 122, wherein the mutation frequency is determined from a linkage database.

134. The method of claim 122, wherein the mutation frequency is determined from a splice variant database.

135. The method of claim 122, wherein the mutation frequency is determined from a translocation database.

136. The method of claim 122, wherein the mutation frequency is determined from a database of known mutations.

137. The method of claim 122, wherein the mutation frequency is further adjusted for wild type genes.

138. The method of claim 122, wherein the mutation frequency is further adjusted for engineered or non-naturally occurring genes.

139. The method of claim 122, wherein the mutation frequency is further adjusted for conservative polymorphisms.

140. The method of claim 122, wherein the mutation frequency is further adjusted for non-conservative polymorphisms.

141. The method of claim 122, wherein the mutation frequency is further adjusted for cDNA stability.

142. The method of claim 122, wherein the mutation frequency is further adjusted for predicted DNA structure.

143. The method of claim 122, wherein the mutation frequency is further adjusted for predicted RNA structure.

144. The method of claim 122, wherein the mutation frequency is further adjusted for predicted protein structure.

145. The method of claim 122, wherein the mutation frequency is further adjusted for post-translational modification sequences.

146. The method of claim 122, wherein the mutation frequency is further adjusted for protein stability.

147. The method of claim 122, wherein the mutation frequency is further adjusted for predicted protein transport.

148. The method of claim 122, wherein the mutation frequency is further adjusted for shuffled genes.

149. The method of claim 122, wherein the mutation frequency is further adjusted for site-directed mutagenesis genes.

150. The method of claim 122, wherein the mutation frequency is further adjusted for methylated sequences

151. The method of claim 122, wherein the mutation frequency is further adjusted for epigenetic variation.

152. The method of claim 122, wherein the mutant genes comprise a cDNA sequence.

153. The method of claim 122, wherein the mutant genes comprise genomic sequence.

154. The method of claim 122, wherein mutant genes comprise an intron/exon boundary.

155. The method of claim 122, wherein mutant genes comprise exons.

156. The method of claim 122, wherein mutant genes comprise other SNPs.

157. The method of claim 122, wherein mutant genes comprise inversions.

158. The method of claim 122, wherein mutant genes comprise deletions.

159. The method of claim 122, wherein mutant genes comprise splice variations.

160. The method of claim 122, wherein mutant genes comprise translocations.

161. The method of claim 122, wherein mutant genes comprise a transcriptional control sequence.

162. The method of claim 122, wherein mutant genes comprise a transport control sequence.

163. The method of claim 122, wherein mutant genes comprise a translational control sequence.

164. The method of claim 122, wherein mutant genes comprise a transcriptional control sequence.

165. The method of claim 122, wherein mutant genes comprise a splicing control sequence.

166. The method of claim 123, wherein in the codon polymorphism predictiveness matrix is normalized for the codon usage of a target organism.

167. The method of claim 123, wherein the codon polymorphism predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database.

168. The method of claim 123, wherein the codon polymorphism predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database minus the known mutant genes of the mutant gene dataset.

169. The method of claim 122, where the codon comprises one or more bases.

170. The method of claim 122, where the codon comprises DNA.

171. The method of claim 122, where the codon comprises RNA.

172. The method of claim 122, where the codon comprises a triplet.

173. The method of claim 122, where the codon comprises a codon.

174. The method of claim 122, where the codon comprises one or more non-sequence base modifications.

175. The method of claim 122, wherein the codon further comprises modifications.

176. The method of claim 122, wherein modifications include methylation or other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid as a whole.

177. The method of claim 122, where the codon comprises an entire genome.

178. The method of claim 122, where the codon comprises a human genome.

179. The method of claim 122, where the codon comprises a gene cluster for a target human disease.

180. The method of claim 122, where the codon polymorphism predictiveness matrix is based on a mutant gene dataset that comprises a human mutation database.

181. The method of claim 122, wherein the step of predicting a likelihood of one or more single nucleotide polymorphisms is determined in silico.

182. A method for creating a variation predictiveness matrix, comprising the steps of:

calculating the variation frequency from a first nucleic acid to a second nucleic acid in a dataset of two or more variations;

determining a variation predictiveness value from the calculated variation frequency; and

generating a variation predictiveness matrix that correlates the frequency of a first to a second nucleic acid with the variation predictiveness value.

183. The method of claim 182, wherein the dataset comprises nucleic acids with chemical modifications.

184. The method of claim 183, wherein the chemical modifications include methylation or other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid as a whole.

185. The method of claim 182, wherein the variation frequency is determined from a variation dataset.

186. A method for creating a polymorphism predictiveness matrix, comprising the steps of:

calculating the mutation frequency from a first codon to a second codon in a dataset of two or more mutant genes;

determining a polymorphism predictiveness value from the calculated mutation frequency; and

generating a codon polymorphism predictiveness matrix that correlates the frequency of a first to a second codon mutation with the polymorphism predictiveness value.

187. The method of claim 186, wherein the dataset comprises nucleic acids with chemical modifications.

188. The method of claim 187, wherein the chemical modifications include methylation or other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid as a whole.

189. The method of claim 186, wherein in the codon polymorphism predictiveness matrix is normalized for the codon usage of a target organism.

190. The method of claim 186, wherein the codon polymorphism predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database.

191. The method of claim 186, wherein the codon polymorphism predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database minus the known mutant genes of the mutant gene dataset.

192. The method of claim 186, wherein the codon comprises one or more bases.

193. The method of claim 186, where the codon comprises a triplet.

194. The method of claim 186, where the codon comprises a codon.

195. The method of claim 186, where the codon comprises one or more non-sequence base modifications.

196. An isolated and purified nucleic acid comprising a predicted single nucleotide variation of a nucleic acid sequence based on the variation predictiveness matrix sequence of claim 1.

197. An isolated and purified nucleic acid comprising a predicted single nucleotide polymorphism of a wild-type gene sequence based on the codon mutation predictiveness matrix sequence of claim 1.

198. An apparatus for detecting a single nucleotide polymorphism comprising:

a substrate; and

one or more isolated and purified nucleic acids comprising a predicted single nucleotide variation of a nucleic acid sequence based on a variation predictiveness matrix sequence affixed to the substrate.

199. The apparatus of claim 198, wherein the substrate comprises a microfabricated solid surface to which molecules may be attached through either covalent or non-covalent bonds.

200. The apparatus of claim 198, wherein the substrate further comprises Langmuir-Bodgett films, glass, functionalized glass, germanium, silicon, PTFE, polystyrene, gallium arsenide, gold, silver, or any materials comprising amino, carboxyl, thiol or hydroxyl functional groups incorporated on a planar or spherical surface.

201. An apparatus for detecting a single nucleotide polymorphism comprising:

a substrate; and

one or more isolated and purified nucleic acids comprising a predicted single nucleotide polymorphism of a wild-type gene sequence based on a codon polymorphism predictiveness matrix. sequence affixed to the substrate.

202. The apparatus of claim 201, wherein the substrate comprises a microfabricated solid surface to which molecules may be attached through either covalent or non-covalent bonds.

203. A computer program embodied on a computer readable medium for predicting variations, comprising:

a code segment for creating variation predictiveness matrix from a nucleic acid dataset;

a code segment for comparing a wild-type gene sequence with the variation predictiveness matrix; and

a code segment for predicting variations in the wild-type gene sequence based on the comparison.

204. A computer program embodied on a computer readable medium for predicting polymorphisms, comprising:

a code segment for creating a codon mutation predictiveness matrix from a mutant gene dataset;

a code segment for comparing a wild-type gene sequence with the codon polymorphism predictiveness matrix; and

a code segment for predicting polymorphisms in the wild-type gene sequence based on the comparison.

205. A polymorphism prediction dataset, comprising:

a first nucleic acid;

a second nucleic acid variation that correlates to a polymorphism from the first nucleic acid; and

a variation predictiveness value determined from known variations in a variation database for a target organism.

206. A polymorphism prediction dataset, comprising:

a first codon;

a second codon mutation that correlates to a mutation from the first codon; and

a codon polymorphism predictiveness value determined from known mutations in a mutation database for a target organism.

207. A single nucleotide polymorphism determined by the method of claim 1.

208. A method for predicting single nucleotide polymorphisms, comprising the steps of:

inputing each codon in a queried nucleic acid sequence;

determining each possible nonsynonymous mutation;

assigning a predictiveness value to that mutation based on the identity of the wild-type and resultant codon; and

ranking of all predictiveness values to highlight the likely to occur and impact gene function.

209. The method of claim 208, further comprising the steps of:

parsing one or more nucleic acid sequence input files having sequence information;

calculating an expected mutation liklihood according to a user-defined threshold; and

ranking of point mutation predictions by a ζ-value.

210. The method of claim 208, further comprising the step of generating a delimited file suitable for a standard spreadsheet application.

211. An isolated and purified nucleic acid comprising SEQ ID NOS.: 1-12.

212. An isolated and purified nucleic acid comprising a cardiomyopathy disease related SNP selected from the group consisting essentially of BDKRB2, EDNRA, ADRB1, ADRB2, CREB1 and MCIP.

213. An isolated and purified nucleic acid of claim 211, wherein the SNP is Thr->Met substitution in BDKRB2 at position 383.